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* You should state whether an appropriate sample size was computed when the study was being designed
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Raw barcode sequencing data are available from the NIH Sequence Read Archive as accession PRJNA630095 (<https://trace.ncbi.nlm.nih.gov/Traces/study/?acc=SRP259652>). Barcode sequences, counts, fitness values, and PPI calls are available in the Supplementary Tables (<https://osf.io/jmhrb/>). Additional data to make figures are available in Mendeley data (<https://data.mendeley.com/datasets/9ygwhk5cs3/2>) and Open Science Framework (<https://osf.io/7yt59/>) as detailed in code repository README files. Analysis scripts are written in R and Python. All code used to analyze data, perform statistical analyses, and generate figures is available at Github (<https://github.com/sashaflevy/PPiSeq>).